Amendments to the Claim:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Previously Presented) A method for estimating the skin cancer, lung cancer, breast cancer and colon cancer risk of an individual comprising

- assessing in the genetic material of a sample from said individual a sequence polymorphism

- in a region corresponding to SEQ ID NO: 2, or a part thereof, or
- in a region complementary to SEQ ID NO: 2, or a part thereof, or
- in a transcription product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof, or
- or translation product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof,
- obtaining a sequence polymorphism response,

- estimating the skin cancer, lung cancer, breast cancer and colon cancer risk of said individual based on the sequence polymorphism response.

2. (Original) The method according to claim 1, wherein a sequence polymorphism is assessed

- in a region corresponding to SEQ ID NO: 1, or a part thereof, or
- in a region complementary to SEQ ID NO: 1, or a part thereof, or
- in a transcription product from a sequence in a region corresponding to SEQ ID NO: 1, or a part thereof, or

- or translation product from a sequence in a region corresponding to SEQ ID NO: 1, or a part thereof.

3. (Previously Presented) The method according to claim 1, wherein the cell sample is a blood sample, a tissue sample, a sample of secretion, semen, ovum, a washing of a body surface, or a clipping of a body surface.

4. (Previously Presented) The method according to claim 1, wherein the cell is selected from white blood cells and tumor tissue.

5. (Previously Presented) The method according to claim 1, wherein the sequence polymorphism comprises at least one mutation base change.

6. (Previously Presented) The method according to claim 1, wherein the sequence polymorphism comprises at least two base changes.

7. (Previously Presented) The method according to claim 1, wherein the sequence polymorphism comprises at least one single nucleotide polymorphism.

8. (Previously Presented) The method according to claim 1, wherein the sequence polymorphism comprises at least two single nucleotide polymorphisms.

9. (Previously Presented) The method according to claim 1, wherein the sequence polymorphism comprises at least one tandem repeat polymorphism.

10. (Previously Presented) The method according to claim 1, wherein the sequence polymorphism comprises at least two tandem repeat polymorphisms.

11-14 (cancelled)

15. (Previously Presented) The method according to claim 1, wherein the assessment is conducted by means of at least one nucleic acid primer or probe.

16. (Original) The method according to claim 15, wherein the nucleotide primer or probe is capable of hybridising to a subsequence of the region corresponding to SEQ ID NO: 1, or a part thereof, or a region complementary to SEQ ID NO:1.

17. (Original) The method according to claim 15, wherein the primer or probe has a length of at least 9 nucleotide or peptide monomers.

18. (Currently Amended) The method according to claim ~~11~~ 15, wherein at least one primer or probe is capable of hybridising to a subsequence selected from the group of subsequences consisting of

1. GCTCTGAAAC TTACTAGCCC(A/G)GTATTTATGG AGAGGCATTT (SEQ ID NO:3)
2. GTGGTCAAAT TCTCATTCAT CGTGG (T/C) CCAGGCAAGC ACACTTCCTC (SEQ ID NO:4)
3. ACCCTGAGGT GAGCACCTGT TCCTT(C/T) TCCTTGCCCT TAGCCCAGAG GTAGA (SEQ ID NO:5)
4. GGGCAGGGGT TTGTGCCTCC AATGA (G/A) CACAAGCTCC CCCTGCCCCC CAACT (SEQ ID NO:6)
5. CCTGGCGGTG GCCGTCACCA GCTTT (T/C) GGGGGTGTTT GGGAAGCTGG (SEQ ID NO:75
6. CTCCAGCCCC ACTGTTCCCT (A/G) GGCCCTATTG GTCCCCCTGG (SEQ ID NO:76)
7. ACAAGGAGGA GGCAGAAGTG AGGTT (G/C) AAACCCACTG CCCAATCTTA (SEQ ID NO:77)
8. CCAACACGGT GAAACCCCGT CTGTA(T/C)TAAAAATACA AAAATTAGCC (SEQ

ID NO:78)

9. AATCCAGGAC CCCATAATCT TCCGT (C/T) ATCTAAAACA ATAATGGTGA (SEQ ID NO:79)

10. CCCAAGGGGG CGAGGGGAGG GTGAA (A/G) GGGTGGGACG GGGGCAGCCG (SEQ ID NO:80)

11. GAAGTGAGAA GGGGGCTGGG GGTCG (G/-) CGCTCGCTAG CGGGCGCGGG (SEQ ID NO:81)

12. CGCACGCGCA GTATCCCGAT TGGCT (C/G) TGCCCTAGCG GATTGACGGG (SEQ ID NO:82)

13. AACTCCTGGG TTCGATCAAT ACTCA (GACA/-) ATCTTGGCAG GCGCAGGAGG (SEQ ID NO:83)

14. GCTGGGATTA CAGGCTTGAG CCACC (A/G) CGCCCGGCCT GCAAAGCCAT (SEQ ID NO:84)

15. TTTTGTATCT TTAGTAGAGA CAGG (T/G) TTTCTCCATG TTGGTCAGGC (SEQ ID NO:85)

16. GCCTCAGCCT CCCGAGTAGC TGAGACT (C/A) CAGGTGCCCG CCACCACGCC (SEQ ID NO:86)

17. TGAAATTGTA GGTTGAGAGG CCAGGCG (C/T) GGTGCTCACG CCTGTAATTT (SEQ ID NO:87)

18. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT (SEQ ID NO:88)

19. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG (SEQ ID NO:89)

20. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT (SEQ ID NO:90)

21. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC (SEQ ID NO:91)

22. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG (SEQ ID NO:92)

23. TCTTAGGACG CATGGGGGT (T/G) GAGAGAACGG GGAGATAGAC (SEQ ID NO:93)

24. CTGGGTTCTA GAACTACC (C/T) ATGCAAACCC AGCTGTTTCC (SEQ ID NO:94)

25. ATTCTGCCCT GGGTTCTAGA ACTACCT (C/A) TGCAAACCCA GCTGTTTCCC (SEQ ID NO:95)

26. GCTGTTTCCC ACCCCATAAG GCA (A/G) TAGGGGAGCC CACCTCCGCC (SEQ ID NO:96)
27. GACCTAGAAG ATCGGTCGAG A (C/T) AGCAGCTTGA GGCTGGCAGG (SEQ ID NO:97)
28. CTGGCCAGGA ATGCAGTCGG GTCAC (C/T) CTGTCTAGCC ACCGTCTCGC (SEQ ID NO:98)
29. GGGAGGAGTC GCCGATCAGG (C/T) CCCTTCCTGA AAGTCATCGA (SEQ ID NO:99)
30. GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG (SEQ ID NO:100)
31. TAGAAATACT AACAAAGGGC (T/C) GTGGGTTTCT CCCCCTGCTT (SEQ ID NO:101)
32. ACAGGAGAGG GAAGGTTTTTTG (A/T) TTTTTTTTTT GTTTTTTTTT (SEQ ID NO:102)
33. GAAGAGGAAG AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCAGAAG (SEQ ID NO:103)
34. GCGCCTCAAC AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGGCAGCT (SEQ ID NO:213)
35. TTGAGACTCT CTGTTTGAT (A/G) CTTCACTCAG AAGGTGCTTC (SEQ ID NO:105)
36. AGGCCAGGCT CCTGCTGGCT G (C/G) GCTGGTGCAG TCTCTGGGGA (SEQ ID NO:106)
37. CCCCTATACC CTCAAGCAT (C/T) TATCCATTGA GTTACAAACA (SEQ ID NO:107) and
38. ACCATCCCCC GCCTTCCGTT (A/C) GTCCGGCCCC CGAGGCTAGC (SEQ ID NO:108),

or to a sequence complementary to any of the subsequences 1 to 38 (SEQ ID NOs:1-6, 75-108) above.

19. (Previously Presented) The method according to claim 18, wherein at least one nucleotide probe is selected from the group consisting of

1. TGAAATTGTA GGTTGAGAGG CCAGGCG (C/T) GGTGCTCACG CCTGTAATTT

(SEQ ID NO:87)

2. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT (SEQ ID NO:88)

3. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG (SEQ ID NO:89)

4. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT (SEQ ID NO:90)

5. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC (SEQ ID NO:91)

6. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG (SEQ ID NO:92)

7. TCTTAGGACG CATGGGGGT (T/G) GAGAGAACGG GGAGATAGAC (SEQ ID NO:93)

8. CTGGGTTCTA GAACTACC (C/T) ATGCAAACCC AGCTGTTTCC (SEQ ID NO:94)

9. ATTCTGCCCT GGGTTCTAGA ACTACCT (C/A) TGCAAACCCA GCTGTTTCCC (SEQ ID NO:95)

10. GCTGTTTCCC ACCCCATAAG GCA (A/G) TAGGGGAGCC CACCTCCGCC (SEQ ID NO:96)

11. GACCTAGAAG ATCGGTCGAG A (C/T) AGCAGCTTGA GGCTGGCAGG (SEQ ID NO:97)

12. CTGGCCAGGA ATGCAGTCGG GTCAC (C/T) CTGTCTAGCC ACCGTCTCGC (SEQ ID NO:98)

13. GGGAGGAGTC GCCGATCAGG (C/T) CCCTTCCTGA AAGTCATCGA (SEQ ID NO:99)

14. GCAGCCCGGG CTACAGGGTT (A/G) CCTGAGGTGT GGGTCCCAGG (SEQ ID NO:100)

15. TAGAAATACT AACAAAGGGC (T/C) GTGGGTTTCT CCCCCTGCTT (SEQ ID NO:101)

16. ACAGGAGAGG GAAGGTTTTTTG (A/T) TTTTTTTTTT GTTTTTTTTT (SEQ ID NO:102)

17. GAAGAGGAAG AAGCCCAAAG GGA (A/C) AGAAACCTTC GAGCCAGAAG (SEQ ID NO:103) and

18. GCGCCTCAAC AGCCAGAAGG AGCG (A/G) AGCCTCAGGC CCAGGCAGCT (SEQ ID NO:213),

or to a sequence complementary to any of the subsequences 1 to 18 (SEQ ID NOs:87-103, 213) above.

20. (Previously Presented) The method according to claim 19, wherein at least one nucleotide probe is selected from the group consisting of

1. GTTTATAAAC ATTAAACCAG (T/A) GCTGTGTGAA GGCACTTAAT (SEQ ID NO:88)
2. CCGTCTCTAT TAAAAATATA AAA (A/C) AATTTAGCCG GGTGTAGCGG (SEQ ID NO:89)
3. GGGAGGCTCG AGGCGGGC (A/G) GATTGCATGA GCTCAGGATT (SEQ ID NO:90)
4. TCCCAAGTTT CAGGGCCCAA (T/G) ATTCTCAAAT CACAGGATTC (SEQ ID NO:91) and
5. TGCAGTGAGC TGAGATCGC (A/G) CCACTGCACT CCAGCCTGGG, (SEQ ID NO:92)

or to a sequence complementary to any of said subsequences.

21. (Previously Presented) The method according to claim 1, wherein at least one sequence polymorphism is assessed in a region corresponding to SEQ ID NO: 1 position 1521-37752 (r).

22. (Previously Presented) The method according to claim 1, wherein at least one sequence polymorphism is assessed in a region corresponding to SEQ ID NO: 1 position 7760-22885 (RAI).

23. (Previously Presented) The method according to claim 1, wherein at least one sequence polymorphism is assessed in a region corresponding to SEQ ID NO: 1 position 34391- 37752.

24. (Previously Presented) The method according to claim 16, wherein at least two different probes are used, one probe being selected from the probes as defined in claim 16, and the other probe being capable of hybridising to a sequence different from

SEQ ID NO: 1, or a part thereof, or to a sequence complementary to a region different from SEQ ID NO: 1, or a part thereof.

25. (Withdrawn) The method according to claim 1, wherein the translational product from a sequence in a region corresponding to SEQ ID NO: 1, or a part thereof, is an antibody.

26. (Withdrawn) A method for estimating the disease prognosis of an individual comprising

- providing a sample from said individual,

- assessing in the genetic material in said sample a sequence polymorphism

- in a region corresponding to SEQ ID NO: 2, or a part thereof, or
- in a region complementary to SEQ ID NO: 2, or a part thereof, or
- in a transcription product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof, or
- or translation product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof,
- obtaining a sequence polymorphism response,

- estimating the disease prognosis of said individual based on the sequence polymorphism response.

27. (Withdrawn) The method according to claim 26, wherein the method further comprises assessing in the genetic material in said sample a sequence polymorphism in

a region corresponding to SEQ ID NO: 1, or a part thereof, or
a region complementary to SEQ ID NO: 1, or a part thereof, or
a transcription product from a sequence in a region corresponding

to SEQ ID NO: 1, or a part thereof, or
a translation product from a sequence in a region corresponding to SEQ ID NO: 1, or a part thereof.

28. (Withdrawn) A method for estimating a treatment response of an individual suffering from cancer to a disease treatment, comprising

- providing a sample from said individual,

- assessing in the genetic material in said sample from said individual a sequence polymorphism

- in a region corresponding to SEQ ID NO: 1, or a part thereof, or
- in a region complementary to SEQ ID NO: 1, or a part thereof, or
- in a transcription product from a sequence in a region corresponding to SEQ ID NO: 1, or a part thereof, or
- or translation product from a sequence in a region corresponding to SEQ ID NO: 1, or a part thereof,
- obtaining a sequence polymorphism response,

- estimating the individual's response to the disease treatment based on the sequence polymorphism response.

29. (Withdrawn) The method according to claim 28, wherein the method further comprises

assessing in the genetic material of a sample from said individual a sequence polymorphism in

(i) a region corresponding to SEQ ID NO: 2, or a part thereof, or
(ii) a region complementary to SEQ ID NO: 2, or a part thereof,

or

(iii) a transcription product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof, or

(iv) a translation product from a sequence in a region corresponding to SEQ ID NO: 2, or a part thereof.

30. (Withdrawn) A primer or probe for detecting polymorphisms for use in a method as defined in claim 1, said primer or probe being selected from the group consisting of

TGGCTAACACGGTGAAACC(SEQ ID NO:7)
GGAATCCAAAGATTCTATGATGG(SEQ ID NO:8)
GGGAGGCGGAGCTTGCAGTGA (SEQ ID NO:9)
CTGAGATCGCACCACTGCAC (SEQ ID NO:10)
GGTTTTCTGCTCTGCACACG (SEQ ID NO:11)
CCTTTCTCCTTCCACCAACG (SEQ ID NO:12)
CGGGCTACAGGGTTACCTGAG (SEQ ID NO:13)
TCTGCAACCTGGTGCGAGCAGC (SEQ ID NO:14)
CCTACCACCATCATCACATCC (SEQ ID NO:15)
GCCTTGCCAAAAATCATAACC (SEQ ID NO:16)
CCTCTCCCCAATTAAGTGCCTTCACACAGC (SEQ ID NO:17)
AGCCAGGGAGGTTGAGGCT (SEQ ID NO:18)
AGACAGCCCTGAATCAGCAC (SEQ ID NO:19)
GCAATGAGCCGAGATAGAA (SEQ ID NO:20) and
TGGCTAGCCCATTACTCTA (SEQ ID NO:21).

31 (Cancelled)

32. (Withdrawn) The primer or probe according to claim 30, wherein the probe is operably linked to at least one label.

33. (Withdrawn) The probe according to claim 30, wherein the

label is selected from the group consisting of TEX, TET, TAM, ROX, R6G, ORG, HEX, FLU, FAM, DABSYL, Cy7, Cy5, Cy3, BOFL, BOF, BO-X, BO-TRX, BO-TMR, JOE, 6JOE, VIC, 6FAM, LCRed640, LCRed705, TAMRA, Biotin, Digoxigenin, DuO-family, Daq-family.

34. (Withdrawn - Currently Amended) The ~~primer or probe~~ method according to claim 26, wherein the primer or probe is operably linked to a surface.

35. (Withdrawn - Currently Amended) The ~~primer or probe~~ method according to claim 34, wherein the surface is the surface of microbeads or a DNA chip.

36 (Cancelled)

37. (Withdrawn - Currently Amended) A kit, comprising at least one primer or probe, said primer or probe being as defined in claim 30, and optionally comprising further amplifying means for nucleic acid amplification.